

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/559,438
Source: IFWP
Date Processed by STIC: 12/16/2005

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,438

TIME: 15:35:24

Input Set : A:\ALEX-P01-107.seq.txt

Output Set : N:\CRF4\12162005\J559438.raw

3 <110> APPLICANT: McWhirter, John
 5 <120> TITLE OF INVENTION: CELL SURFACE PROTEIN ASSOCIATED WITH HUMAN CHRONIC
 LYMPHOCYTIC
 6 LEUKEMIA
 8 <130> FILE REFERENCE: 107 PCT (1087-86 PCT)
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/559,438
 C--> 11 <141> CURRENT FILING DATE: 2005-12-02
 13 <150> PRIOR APPLICATION NUMBER: US 60/530,094
 14 <151> PRIOR FILING DATE: 2003-12-15
 16 <150> PRIOR APPLICATION NUMBER: US 60/475,156
 17 <151> PRIOR FILING DATE: 2003-06-02
 19 <160> NUMBER OF SEQ ID NOS: 86
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 183
 25 <212> TYPE: PRT
 26 <213> ORGANISM: human
 28 <400> SEQUENCE: 1
 30 Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
 31 1 5 10 15
 34 Val Pro Val Gly Arg Gly Asn Tyr Glu Glu Leu Glu Asn Ser Gly Asp
 35 20 25 30
 38 Thr Thr Val Glu Ser Glu Arg Pro Asn Lys Val Thr Ile Pro Ser Thr
 39 35 40 45
 42 Phe Ala Ala Val Thr Ile Lys Glu Thr Leu Asn Ala Asn Ile Asn Ser
 43 50 55 60
 46 Thr Asn Phe Ala Pro Asp Glu Asn Gln Leu Glu Phe Ile Leu Met Val
 47 65 70 75 80
 50 Leu Ile Pro Leu Ile Leu Leu Val Leu Leu Leu Ser Val Val Phe
 51 85 90 95
 54 Leu Ala Thr Tyr Lys Arg Lys Arg Thr Lys Gln Glu Pro Ser Ser
 55 100 105 110
 58 Gln Gly Ser Gln Ser Ala Leu Gln Thr Tyr Glu Leu Gly Ser Glu Asn
 59 115 120 125
 62 Val Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile
 63 130 135 140
 66 Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala
 67 145 150 155 160
 70 Asp Phe Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Ser Asn His
 71 165 170 175
 74 Asn Pro Ser Asp Ser Glu Ser
 75 180
 78 <210> SEQ ID NO: 2
 79 <211> LENGTH: 675

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Input Set : A:\ALEX-P01-107.seq.txt

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80 <212> TYPE: DNA
81 <213> ORGANISM: human
83 <400> SEQUENCE: 2
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86 tccccgcgca gccctagtct tcgccctggg gatcgcgctc gttcccgtcg gccggggtaa    120
88 ttatgaggaa ttagaaaact caggagatac aactgtggaa tctgaaagac caaataaagt    180
90 gactattcca agcacatttg ctgcagtgc catcaaagaa acattaaatg caaatataaa    240
92 ttctaccaac tttgctcgg atgaaaatca gttagagttt atactgatgg tgtaaatccc    300
94 attgatttta ttggtcctct tactttttatc cgtgggtattc cttgcaacat actataaaaag  360
96 aaaaagaact aacaagaacc ttctagccaa ggatctcaga gtgctttaca gacatatgaa    420
98 ctgggaagtg aaaacgtgaa agtccttatt tttgaggaag atacaccctc tgttatggaa    480
100 attgaaatgg aagagcttga taaatggatg aacagcatga atagaaatgc cgactttgaa    540
102 tgtttacctt ccttgaagga agagaaggaa tcaaatcaca acccaagtga cagtgaatcc    600
104 taaacctgaa tggcgctcat gttttccaag agaagcagcc cctgagggag tctgctgagg    660
106 ctgccaacag gatcc                                          675
109 <210> SEQ ID NO: 3
110 <211> LENGTH: 181
111 <212> TYPE: PRT
112 <213> ORGANISM: murine
114 <400> SEQUENCE: 3
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117 1          5          10          15
120 Gly Gln Ser Ser Gln Gly Asn Asp Glu Glu Ser Glu Tyr Ser Gly Gln
121          20          25          30
124 Ser Ile Thr Glu Glu Glu Asn Ser Glu Asp Glu Thr Thr Arg Ser Ala
125          35          40          45
128 Leu Ala Thr Val Thr Thr Glu Ala Leu Ala Glu Asn Val Asn Ser Thr
129          50          55          60
132 His Thr Asn Asp Thr Ser Asn Gln Val Glu Phe Ile Leu Met Val Ala
133 65          70          75          80
136 Ile Pro Leu Ala Ala Leu Leu Ile Leu Leu Phe Met Val Leu Ile Ala
137          85          90          95
140 Thr Tyr Phe Lys Ser Lys Arg Pro Lys Gln Glu Pro Ser Ser Gln Gly
141          100         105         110
144 Ser Gln Ser Ala Leu Gln Thr His Glu Leu Gly Gly Glu Thr Leu Lys
145          115         120         125
148 Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile Glu Met
149          130         135         140
152 Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala Asp Tyr
153 145         150         155         160
156 Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Pro Asn Pro Ser Pro
157          165         170         175
160 Ser Asp Asn Glu Ser
161          180
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 367
166 <212> TYPE: PRT
167 <213> ORGANISM: rat
169 <400> SEQUENCE: 4

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171 Met Thr Arg Pro Pro Tyr Gln Glu Ala Pro Val Gly Asp Leu Gln Met
172 1          5          10          15
175 Gly Asp Arg Gln Glu Ser Ser Gly Asp Lys Asp Arg Asn Asp Glu Asp
176          20          25          30
179 Ser Glu Tyr Ser Gly His Ser Thr Thr Glu Glu Asp Thr Ala Glu Glu
180          35          40          45
183 Glu Thr Thr Arg Ala Leu Ala Thr Val Thr Thr Glu Ala Leu Ala Glu
184          50          55          60
187 Ser Ala Asn Ser Thr His Ile His Gly Thr Ser Asn Gln Val Glu Phe
188 65          70          75          80
191 Ile Leu Met Val Ala Val Pro Leu Ala Ala Leu Leu Ile Leu Leu Phe
192          85          90          95
195 Ala Ile Leu Ile Val Ile Tyr Phe Lys Ser Arg Arg Pro Lys Gln Glu
196          100          105          110
199 Pro Ser Ser Gln Gly Ser Gln Ser Ala Leu Gln Thr Leu Arg Leu Leu
200          115          120          125
203 Leu Ser Leu Glu Thr Lys Arg Pro Glu Pro Ser Val Ala Pro Ser Leu
204          130          135          140
207 Gly Pro Arg Pro Thr Ile Pro Leu Pro Thr Ala Gln Arg Gly Pro Cys
208 145          150          155          160
211 Gln Gln Ser Gly Cys Lys Ala Gly Thr Lys Gly Gly Arg Gln Asp Arg
212          165          170          175
215 Gly Glu Asn Glu Met Ala Gly Arg Lys Gly Thr Lys Trp Lys Pro Val
216          180          185          190
219 Gly Asn Gly Pro Gly Ala Glu Lys Met Arg Pro Gln Lys Ala Phe Cys
220          195          200          205
223 Ser Phe Asn Ala Asp Tyr Gly Ala Ser His Ser Val His Leu Glu His
224          210          215          220
227 Phe Gly Asn Gly Phe Leu Asn Phe Ser Ile Ile Cys Met Gln Val Gly
228 225          230          235          240
231 Phe Cys Pro Pro Pro Ser Leu Trp Gly Ala Gln Met Arg Val Glu Ile
232          245          250          255
235 Arg Ala His Ser Gly Thr Val Glu Pro Leu Ala Val Trp Glu Ile Gly
236          260          265          270
239 Gly Glu Val Ala Lys Gln Gly Lys Gly Thr Asp Asp Leu Gly Gly Glu
240          275          280          285
243 Thr Leu Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu
244          290          295          300
247 Ile Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn
248 305          310          315          320
251 Gly Thr Trp Lys Thr Lys Ala Phe Ala Cys Leu Cys Gly Asn Ala Gly
252          325          330          335
255 Leu Asp Gly Cys Leu Cys Phe Ile Ser Asn Ser Glu Asn Leu Lys Leu
256          340          345          350
259 Cys Phe Ile Trp His Ser Thr Cys Ala Leu Leu Lys Asp Pro Val
260          355          360          365
263 <210> SEQ ID NO: 5
264 <211> LENGTH: 703
265 <212> TYPE: DNA

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266 <213> ORGANISM: artificial sequence

268 <220> FEATURE:

269 <223> OTHER INFORMATION: FLJ32028 with an HA epitope tag

271 <400> SEQUENCE: 5

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272 aagcttagcc cggcgagca tcctgagcgc gcctctgccg aggcgagcgg acatgcaggc      60
274 tccccgcgca gccctagtct tcgccctggt gatcgcgctc gttcccgctc gccggggtaa    120
276 ttatccatat gatgttccag attatgctta tgaggaatta gaaaactcag gagatacaac    180
278 tgtggaatct gaaagaccaa ataaagtacg tattccaagc acatttgctg cagtgaccat    240
280 caaagaaaca ttaaatgcaa atataaattc taccaacttt gctccggatg aaaatcagtt    300
282 agagtttata ctgatggtgt taatcccatt gattttattg gtcctcttac ttttatccgt    360
284 ggtattcctt gcaacatact ataaaagaaa aagaactaaa caagaacctt ctagccaagg    420
286 atctcagagt gctttacaga catatgaact gggaagtga aacgtgaaag tccctatatt    480
288 tgaggaagat acaccctctg ttatggaaat tgaaatggaa gagcttgata aatggatgaa    540
290 cagcatgaat agaaatgccg actttgaatg ttacctacc ttgaaggaag agaaggaatc    600
292 aaatcacaac ccaagtgaca gtgaatccta aacctgaatg gcgctcatgt tttccaagag    660
294 aagcagcccc tgaggaggct tgctgaggct gccaacagga tcc                          703

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297 <210> SEQ ID NO: 6

298 <211> LENGTH: 192

299 <212> TYPE: PRT

300 <213> ORGANISM: artificial sequence

302 <220> FEATURE:

303 <223> OTHER INFORMATION: FLJ32028 with HA epitope tag

305 <400> SEQUENCE: 6

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307 Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
308 1          5          10          15
311 Val Pro Val Gly Arg Gly Asn Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
312          20          25          30
315 Tyr Glu Glu Leu Glu Asn Ser Gly Asp Thr Thr Val Glu Ser Glu Arg
316          35          40          45
319 Pro Asn Lys Val Thr Ile Pro Ser Thr Phe Ala Ala Val Thr Ile Lys
320          50          55          60
323 Glu Thr Leu Asn Ala Asn Ile Asn Ser Thr Asn Phe Ala Pro Asp Glu
324 65          70          75          80
327 Asn Gln Leu Glu Phe Ile Leu Met Val Leu Ile Pro Leu Ile Leu Leu
328          85          90          95
331 Val Leu Leu Leu Leu Ser Val Val Phe Leu Ala Thr Tyr Tyr Lys Arg
332          100         105         110
335 Lys Arg Thr Lys Gln Glu Pro Ser Ser Gln Gly Ser Gln Ser Ala Leu
336          115         120         125
339 Gln Thr Tyr Glu Leu Gly Ser Glu Asn Val Lys Val Pro Ile Phe Glu
340          130         135         140
343 Glu Asp Thr Pro Ser Val Met Glu Ile Glu Met Glu Glu Leu Asp Lys
344 145         150         155         160
347 Trp Met Asn Ser Met Asn Arg Asn Ala Asp Phe Glu Cys Leu Pro Thr
348          165         170         175
351 Leu Lys Glu Glu Lys Glu Ser Asn His Asn Pro Ser Asp Ser Glu Ser
352          180         185         190

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355 <210> SEQ ID NO: 7

356 <211> LENGTH: 637

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Input Set : A:\ALEX-P01-107.seq.txt

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357 <212> TYPE: DNA
358 <213> ORGANISM: artificial sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: FLJ32028 with HA epitope tag
363 <400> SEQUENCE: 7
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366 tccccgcgca gccctagtct tcgccctggt gatcgcgctc gttcccgtcg gccggggtaa      120
368 ttatgaggaa ttagaaaact caggagatac aactgtggaa tctgaaagac caaataaagt      180
370 gactattcca agcacatttg ctgcagtgac catcaaagaa acattaaatg caaatataaa      240
372 ttctaccaac tttgctccgg atgaaaatca gttagagttt atactgatgg tgtaaatccc      300
374 attgatttta ttggtcctct tactttttatc cgtggtattc cttgcaacat actataaaag      360
376 aaaaagaact aaacaagaac ctcttagcca aggatctcag agtgctttac agacatatga      420
378 actgggaagt gaaaacgtga aagtccttat ttttgaggaa gatacacctt ctgttatgga      480
380 aattgaaatg gaagagcttg ataatggat gaacagcatg aatagaaatg ccgactttga      540
382 atgtttacct accttgaagg aagagaagga atcaaatac aaccaagtg acagtgaatc      600
384 ctatccatat gatgttcacg attatgctta aggatcc                                     637
387 <210> SEQ ID NO: 8
388 <211> LENGTH: 192
389 <212> TYPE: PRT
390 <213> ORGANISM: artificial sequence
392 <220> FEATURE:
393 <223> OTHER INFORMATION: FLJ32028 with HA epitope tag
395 <400> SEQUENCE: 8
397 Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
398 1          5          10         15
401 Val Pro Val Gly Arg Gly Asn Tyr Glu Glu Leu Glu Asn Ser Gly Asp
402          20         25         30
405 Thr Thr Val Glu Ser Glu Arg Pro Asn Lys Val Thr Ile Pro Ser Thr
406          35         40         45
409 Phe Ala Ala Val Thr Ile Lys Glu Thr Leu Asn Ala Asn Ile Asn Ser
410          50         55         60
413 Thr Asn Phe Ala Pro Asp Glu Asn Gln Leu Glu Phe Ile Leu Met Val
414 65         70         75         80
417 Leu Ile Pro Leu Ile Leu Leu Val Leu Leu Leu Ser Val Val Phe
418          85         90         95
421 Leu Ala Thr Tyr Tyr Lys Arg Lys Arg Thr Lys Gln Glu Pro Ser Ser
422         100        105        110
425 Gln Gly Ser Gln Ser Ala Leu Gln Thr Tyr Glu Leu Gly Ser Glu Asn
426         115        120        125
429 Val Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile
430        130        135        140
433 Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala
434 145        150        155        160
437 Asp Phe Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Ser Asn His
438        165        170        175
441 Asn Pro Ser Asp Ser Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
442        180        185        190
445 <210> SEQ ID NO: 9
446 <211> LENGTH: 1421

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/559,438

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Input Set : A:\ALEX-P01-107.seq.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 40

Seq#:10; Xaa Pos. 14,220

Seq#:85; Xaa Pos. 3,5,10,13,14,16,17,19,21,32,39,40,42,61,66,67,68,92,120

Seq#:85; Xaa Pos. 172,174,175

VERIFICATION SUMMARY

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Input Set : A:\ALEX-P01-107.seq.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:208
L:2444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
L:2448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:16
L:2452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:32
L:2456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:48
L:2460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:64
L:2464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:80
L:2472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:112
L:2484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:160